

0570  
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OIPE

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/099,700A

DATE: 06/11/2002

TIME: 16:55:56

Input Set : A:\PTO.VSK.txt

Output Set: N:\CRF3\06112002\J099700A.raw

ENTERED

3 <110> APPLICANT: Edwin L. Madison  
 4 Edgar O. Ong  
 6 <120> TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING TRANSMEMBRANE SERINE  
 PROTEASE 7, THE  
 7 ENCODED POLYPEPTIDES AND METHODS BASED THEREON  
 9 <130> FILE REFERENCE: 24745-1613  
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/099,700A  
 C--> 12 <141> CURRENT FILING DATE: 2002-05-24  
 14 <150> PRIOR APPLICATION NUMBER: 60/275,592  
 15 <151> PRIOR FILING DATE: 2001-03-13  
 17 <160> NUMBER OF SEQ ID NOS: 22  
 19 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
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 23 <212> TYPE: DNA  
 24 <213> ORGANISM: Homo Sapien  
 26 <220> FEATURE:  
 27 <221> NAME/KEY: CDS  
 28 <222> LOCATION: (23)...(2589)  
 29 <223> OTHER INFORMATION: Nucleotide sequence encoding MTSP1  
 31 <300> PUBLICATION INFORMATION:  
 32 <301> AUTHORS: O'Brien, T.J. and Tanimoto, H.  
 33 <308> DATABASE ACCESSION NO: GenBank #AR081724  
 34 <309> DATABASE ENTRY DATE: 2000-08-31  
 35 <310> PATENT DOC NO: 5,972,616  
 36 <311> PATENT FILING DATE: 1998-02-20  
 37 <312> PUBLICATION DATE: 1999-10-26  
 39 <400> SEQUENCE: 1  
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 41 Met Gly Ser Asp Arg Ala Arg Lys Gly Gly  
 42 1 5 10  
 44 ggg ggc ccg aag gac ttc ggc gcg gga ctc aag tac aac tcc cgg cac 100  
 45 Gly Gly Pro Lys Asp Phe Gly Ala Gly Leu Lys Tyr Asn Ser Arg His  
 46 15 20 25  
 48 gag aaa gtg aat ggc ttg gag gaa ggc gtg gag ttc ctg cca gtc aac 148  
 49 Glu Lys Val Asn Gly Leu Glu Glu Gly Val Glu Phe Leu Pro Val Asn  
 50 30 35 40  
 52 aac gtc aag aag gtg gaa aag cat ggc ccg ggg cgc tgg gtg gtg ctg 196  
 53 Asn Val Lys Lys Val Glu Lys His Gly Pro Gly Arg Trp Val Val Leu  
 54 45 50 55  
 56 gca gcc gtg ctg atc ggc ctc ctc ttg gtc ttg ctg ggg atc ggc ttc 244  
 57 Ala Ala Val Leu Ile Gly Leu Leu Leu Val Leu Leu Gly Ile Gly Phe  
 58 60 65 70  
 60 ctg gtg tgg cat ttg cag tac cgg gac gtg cgt gtc cag aag gtc ttc 292

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62	75					80					85					90	
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65	Asn	Gly	Tyr	Met	Arg	Ile	Thr	Asn	Glu	Asn	Phe	Val	Asp	Ala	Tyr	Glu	
66					95					100					105		
68	aac	tcc	aac	tcc	act	gag	ttt	gta	agc	ctg	gcc	agc	aag	gtg	aag	gac	388
69	Asn	Ser	Asn	Ser	Thr	Glu	Phe	Val	Ser	Leu	Ala	Ser	Lys	Val	Lys	Asp	
70					110					115					120		
72	gcg	ctg	aag	ctg	ctg	tac	agc	gga	gtc	cca	ttc	ctg	ggc	ccc	tac	cac	436
73	Ala	Leu	Lys	Leu	Leu	Tyr	Ser	Gly	Val	Pro	Phe	Leu	Gly	Pro	Tyr	His	
74			125					130					135				
76	aag	gag	tcg	gct	gtg	acg	gcc	ttc	agc	gag	ggc	agc	gtc	atc	gcc	tac	484
77	Lys	Glu	Ser	Ala	Val	Thr	Ala	Phe	Ser	Glu	Gly	Ser	Val	Ile	Ala	Tyr	
78		140						145					150				
80	tac	tgg	tct	gag	ttc	agc	atc	ccg	cag	cac	ctg	gtg	gag	gag	gcc	gag	532
81	Tyr	Trp	Ser	Glu	Phe	Ser	Ile	Pro	Gln	His	Leu	Val	Glu	Glu	Ala	Glu	
82	155					160					165				170		
84	cgc	gtc	atg	gcc	gag	gag	cgc	gta	gtc	atg	ctg	ccc	ccg	cgg	gcg	cgc	580
85	Arg	Val	Met	Ala	Glu	Glu	Arg	Val	Val	Met	Leu	Pro	Pro	Arg	Ala	Arg	
86					175					180					185		
88	tcc	ctg	aag	tcc	ttt	gtg	gtc	acc	tca	gtg	gtg	gct	ttc	ccc	acg	gac	628
89	Ser	Leu	Lys	Ser	Phe	Val	Val	Thr	Ser	Val	Val	Ala	Phe	Pro	Thr	Asp	
90				190						195				200			
92	tcc	aaa	aca	gta	cag	agg	acc	cag	gac	aac	agc	tgc	agc	ttt	ggc	ctg	676
93	Ser	Lys	Thr	Val	Gln	Arg	Thr	Gln	Asp	Asn	Ser	Cys	Ser	Phe	Gly	Leu	
94			205					210					215				
96	cac	gcc	cgc	ggt	gtg	gag	ctg	atg	cgc	ttc	acc	acg	ccc	ggc	ttc	cct	724
97	His	Ala	Arg	Gly	Val	Glu	Leu	Met	Arg	Phe	Thr	Thr	Pro	Gly	Phe	Pro	
98		220				225					230						
100	gac	agc	ccc	tac	ccc	gct	cat	gcc	cgc	tgc	cag	tgg	gcc	ctg	cgg	ggg	772
101	Asp	Ser	Pro	Tyr	Pro	Ala	His	Ala	Arg	Cys	Gln	Trp	Ala	Leu	Arg	Gly	
102	235					240					245				250		
104	gac	gcc	gac	tca	gtg	ctg	agc	ctc	acc	ttc	cgc	agc	ttt	gac	ctt	gcg	820
105	Asp	Ala	Asp	Ser	Val	Leu	Ser	Leu	Thr	Phe	Arg	Ser	Phe	Asp	Leu	Ala	
106				255						260				265			
108	tcc	tgc	gac	gag	cgc	ggc	agc	gac	ctg	gtg	acg	gtg	tac	aac	acc	ctg	868
109	Ser	Cys	Asp	Glu	Arg	Gly	Ser	Asp	Leu	Val	Thr	Val	Tyr	Asn	Thr	Leu	
110				270					275					280			
112	agc	ccc	atg	gag	ccc	cac	gcc	ctg	gtg	cag	ttg	tgt	ggc	acc	tac	cct	916
113	Ser	Pro	Met	Glu	Pro	His	Ala	Leu	Val	Gln	Leu	Cys	Gly	Thr	Tyr	Pro	
114			285					290					295				
116	ccc	tcc	tac	aac	ctg	acc	ttc	cac	tcc	tcc	cag	aac	gtc	ctg	ctc	atc	964
117	Pro	Ser	Tyr	Asn	Leu	Thr	Phe	His	Ser	Ser	Gln	Asn	Val	Leu	Leu	Ile	
118		300				305					310						
120	aca	ctg	ata	acc	aac	act	gag	cgg	cgg	cat	ccc	ggc	ttt	gag	gcc	acc	1012
121	Thr	Leu	Ile	Thr	Asn	Thr	Glu	Arg	Arg	His	Pro	Gly	Phe	Glu	Ala	Thr	
122	315					320					325				330		
124	ttc	ttc	cag	ctg	cct	agg	atg	agc	agc	tgt	gga	ggc	cgc	tta	cgt	aaa	1060
125	Phe	Phe	Gln	Leu	Pro	Arg	Met	Ser	Ser	Cys	Gly	Gly	Arg	Leu	Arg	Lys	

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128	gcc	cag	ggg	aca	ttc	aac	agc	ccc	tac	tac	cca	ggc	cac	tac	cca	ccc	1108
129	Ala	Gln	Gly	Thr	Phe	Asn	Ser	Pro	Tyr	Tyr	Pro	Gly	His	Tyr	Pro	Pro	
130				350				355				360					
132	aac	att	gac	tgc	aca	tgg	aac	att	gag	gtg	ccc	aac	aac	cag	cat	gtg	1156
133	Asn	Ile	Asp	Cys	Thr	Trp	Asn	Ile	Glu	Val	Pro	Asn	Asn	Gln	His	Val	
134				365				370				375					
136	aag	gtg	agc	ttc	aaa	ttc	ttc	tac	ctg	ctg	gag	ccc	ggc	gtg	cct	gcg	1204
137	Lys	Val	Ser	Phe	Lys	Phe	Phe	Tyr	Leu	Leu	Glu	Pro	Gly	Val	Pro	Ala	
138				380				385				390					
140	ggc	acc	tgc	ccc	aag	gac	tac	gtg	gag	atc	aat	ggg	gag	aaa	tac	tgc	1252
141	Gly	Thr	Cys	Pro	Lys	Asp	Tyr	Val	Glu	Ile	Asn	Gly	Glu	Lys	Tyr	Cys	
142	395					400					405					410	
144	gga	gag	agg	tcc	cag	ttc	gtc	gtc	acc	agc	aac	agc	aac	aag	atc	aca	1300
145	Gly	Glu	Arg	Ser	Gln	Phe	Val	Val	Thr	Ser	Asn	Ser	Asn	Lys	Ile	Thr	
146				415				420						425			
148	gtt	cgc	ttc	cac	tca	gat	cag	tcc	tac	acc	gac	acc	ggc	ttc	tta	gct	1348
149	Val	Arg	Phe	His	Ser	Asp	Gln	Ser	Tyr	Thr	Asp	Thr	Gly	Phe	Leu	Ala	
150				430				435						440			
152	gaa	tac	ctc	tcc	tac	gac	tcc	agt	gac	cca	tgc	ccg	ggg	cag	ttc	acg	1396
153	Glu	Tyr	Leu	Ser	Tyr	Asp	Ser	Ser	Asp	Pro	Cys	Pro	Gly	Gln	Phe	Thr	
154				445				450					455				
156	tgc	cgc	acg	ggg	cgg	tgt	atc	cgg	aag	gag	ctg	cgc	tgt	gat	ggc	tgg	1444
157	Cys	Arg	Thr	Gly	Arg	Cys	Ile	Arg	Lys	Glu	Leu	Arg	Cys	Asp	Gly	Trp	
158				460				465					470				
160	gcc	gac	tgc	acc	gac	cac	agc	gat	gag	ctc	aac	tgc	agt	tgc	gac	gcc	1492
161	Ala	Asp	Cys	Thr	Asp	His	Ser	Asp	Glu	Leu	Asn	Cys	Ser	Cys	Asp	Ala	
162	475					480					485					490	
164	ggc	cac	cag	ttc	acg	tgc	aag	aac	aag	ttc	tgc	aag	ccc	ctc	ttc	tgg	1540
165	Gly	His	Gln	Phe	Thr	Cys	Lys	Asn	Lys	Phe	Cys	Lys	Pro	Leu	Phe	Trp	
166				495				500						505			
168	gtc	tgc	gac	agt	gtg	aac	gac	tgc	gga	gac	aac	agc	gac	gag	cag	ggg	1588
169	Val	Cys	Asp	Ser	Val	Asn	Asp	Cys	Gly	Asp	Asn	Ser	Asp	Glu	Gln	Gly	
170				510				515						520			
172	tgc	agt	tgt	ccg	gcc	cag	acc	ttc	agg	tgt	tcc	aat	ggg	aag	tgc	ctc	1636
173	Cys	Ser	Cys	Pro	Ala	Gln	Thr	Phe	Arg	Cys	Ser	Asn	Gly	Lys	Cys	Leu	
174				525				530					535				
176	tcg	aaa	agc	cag	cag	tgc	aat	ggg	aag	gac	gac	tgt	ggg	gac	ggg	tcc	1684
177	Ser	Lys	Ser	Gln	Gln	Cys	Asn	Gly	Lys	Asp	Asp	Cys	Gly	Asp	Gly	Ser	
178				540				545					550				
180	gac	gag	gcc	tcc	tgc	ccc	aag	gtg	aac	gtc	gtc	act	tgt	acc	aaa	cac	1732
181	Asp	Glu	Ala	Ser	Cys	Pro	Lys	Val	Asn	Val	Val	Thr	Cys	Thr	Lys	His	
182	555					560					565					570	
184	acc	tac	cgc	tgc	ctc	aat	ggg	ctc	tgc	ttg	agc	aag	ggc	aac	cct	gag	1780
185	Thr	Tyr	Arg	Cys	Leu	Asn	Gly	Leu	Cys	Leu	Ser	Lys	Gly	Asn	Pro	Glu	
186				575				580						585			
188	tgt	gac	ggg	aag	gag	gac	tgt	agc	gac	ggc	tca	gat	gag	aag	gac	tgc	1828
189	Cys	Asp	Gly	Lys	Glu	Asp	Cys	Ser	Asp	Gly	Ser	Asp	Glu	Lys	Asp	Cys	
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196	acg	gat	gcg	gat	gag	ggc	gag	tgg	ccc	tgg	cag	gta	agc	ctg	cat	gct	1924
197	Thr	Asp	Ala	Asp	Glu	Gly	Glu	Trp	Pro	Trp	Gln	Val	Ser	Leu	His	Ala	
198		620					625				630						
200	ctg	ggc	cag	ggc	cac	atc	tgc	ggt	gct	tcc	ctc	atc	tct	ccc	aac	tgg	1972
201	Leu	Gly	Gln	Gly	His	Ile	Cys	Gly	Ala	Ser	Leu	Ile	Ser	Pro	Asn	Trp	
202	635					640					645					650	
204	ctg	gtc	tct	gcc	gca	cac	tgc	tac	atc	gat	gac	aga	gga	ttc	agg	tac	2020
205	Leu	Val	Ser	Ala	Ala	His	Cys	Tyr	Ile	Asp	Asp	Arg	Gly	Phe	Arg	Tyr	
206					655					660					665		
208	tca	gac	ccc	acg	cag	tgg	acg	gcc	ttc	ctg	ggc	ttg	cac	gac	cag	agc	2068
209	Ser	Asp	Pro	Thr	Gln	Trp	Thr	Ala	Phe	Leu	Gly	Leu	His	Asp	Gln	Ser	
210				670					675					680			
212	cag	cgc	agc	gcc	cct	ggg	gtg	cag	gag	cgc	agg	ctc	aag	cgc	atc	atc	2116
213	Gln	Arg	Ser	Ala	Pro	Gly	Val	Gln	Glu	Arg	Arg	Leu	Lys	Arg	Ile	Ile	
214			685						690					695			
216	tcc	cac	ccc	ttc	ttc	aat	gac	ttc	acc	ttc	gac	tat	gac	atc	gcg	ctg	2164
217	Ser	His	Pro	Phe	Phe	Asn	Asp	Phe	Thr	Phe	Asp	Tyr	Asp	Ile	Ala	Leu	
218		700					705				710						
220	ctg	gag	ctg	gag	aaa	ccg	gca	gag	tac	agc	tcc	atg	gtg	cgg	ccc	atc	2212
221	Leu	Glu	Leu	Glu	Lys	Pro	Ala	Glu	Tyr	Ser	Ser	Met	Val	Arg	Pro	Ile	
222	715					720					725					730	
224	tgc	ctg	ccg	gac	gcc	tcc	cat	gtc	ttc	cct	gcc	ggc	aag	gcc	atc	tgg	2260
225	Cys	Leu	Pro	Asp	Ala	Ser	His	Val	Phe	Pro	Ala	Gly	Lys	Ala	Ile	Trp	
226					735					740					745		
228	gtc	acg	ggc	tgg	gga	cac	acc	cag	tat	gga	ggc	act	ggc	gcg	ctg	atc	2308
229	Val	Thr	Gly	Trp	Gly	His	Thr	Gln	Tyr	Gly	Gly	Thr	Gly	Ala	Leu	Ile	
230				750					755					760			
232	ctg	caa	aag	ggt	gag	atc	cgc	gtc	atc	aac	cag	acc	acc	tgc	gag	aac	2356
233	Leu	Gln	Lys	Gly	Glu	Ile	Arg	Val	Ile	Asn	Gln	Thr	Thr	Cys	Glu	Asn	
234			765					770					775				
236	ctc	ctg	ccg	cag	cag	atc	acg	ccg	cgc	atg	atg	tgc	gtg	ggc	ttc	ctc	2404
237	Leu	Leu	Pro	Gln	Gln	Ile	Thr	Pro	Arg	Met	Met	Cys	Val	Gly	Phe	Leu	
238		780					785				790						
240	agc	ggc	ggc	gtg	gac	tcc	tgc	cag	ggt	gat	tcc	ggg	gga	ccc	ctg	tcc	2452
241	Ser	Gly	Gly	Val	Asp	Ser	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Ser	
242	795					800					805					810	
244	agc	gtg	gag	gcg	gat	ggg	cgg	atc	ttc	cag	gcc	ggt	gtg	gtg	agc	tgg	2500
245	Ser	Val	Glu	Ala	Asp	Gly	Arg	Ile	Phe	Gln	Ala	Gly	Val	Val	Ser	Trp	
246					815					820					825		
248	gga	gac	ggc	tgc	gct	cag	agg	aac	aag	cca	ggc	gtg	tac	aca	agg	ctc	2548
249	Gly	Asp	Gly	Cys	Ala	Gln	Arg	Asn	Lys	Pro	Gly	Val	Tyr	Thr	Arg	Leu	
250				830					835					840			
252	cct	ctg	ttt	cgg	gac	tgg	atc	aaa	gag	aac	act	ggg	gta	ta	ggggccgggg	2599	
253	Pro	Leu	Phe	Arg	Asp	Trp	Ile	Lys	Glu	Asn	Thr	Gly	Val				
254			845					850					855				
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257 ggctggagac tggaccgctg actgcaccag cgccccaga acatacactg tgaactcaat 2719
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259 gggaggtaga aggggaggac actggtggtt ctactgaccc aactgggggc aaaggtttga 2839
260 agacacagcc tccccgcca gccccaagct gggccgaggc gcgtttgtgt atatctgcct 2899
261 cccctgtctg taaggagcag cgggaacgga gcttcggagc ctcctcagtg aaggtggtgg 2959
262 ggctgccgga tctgggctgt ggggcccttg ggccacgctc ttgaggaagc ccaggctcgg 3019
263 aggaccctgg aaaacagacg ggtctgagac tgaaattgtt ttaccagctc ccagggtgga 3079
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265 aaaaaaaaaa 3147
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269 <212> TYPE: PRT
270 <213> ORGANISM: Homo Sapien
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275 Gly Ala Gly Leu Lys Tyr Asn Ser Arg His Glu Lys Val Asn Gly Leu
276 20 25 30
277 Glu Glu Gly Val Glu Phe Leu Pro Val Asn Asn Val Lys Lys Val Glu
278 35 40 45
279 Lys His Gly Pro Gly Arg Trp Val Val Leu Ala Ala Val Leu Ile Gly
280 50 55 60
281 Leu Leu Leu Val Leu Leu Gly Ile Gly Phe Leu Val Trp His Leu Gln
282 65 70 75 80
283 Tyr Arg Asp Val Arg Val Gln Lys Val Phe Asn Gly Tyr Met Arg Ile
284 85 90 95
285 Thr Asn Glu Asn Phe Val Asp Ala Tyr Glu Asn Ser Asn Ser Thr Glu
286 100 105 110
287 Phe Val Ser Leu Ala Ser Lys Val Lys Asp Ala Leu Lys Leu Leu Tyr
288 115 120 125
289 Ser Gly Val Pro Phe Leu Gly Pro Tyr His Lys Glu Ser Ala Val Thr
290 130 135 140
291 Ala Phe Ser Glu Gly Ser Val Ile Ala Tyr Tyr Trp Ser Glu Phe Ser
292 145 150 155 160
293 Ile Pro Gln His Leu Val Glu Glu Ala Glu Arg Val Met Ala Glu Glu
294 165 170 175
295 Arg Val Val Met Leu Pro Pro Arg Ala Arg Ser Leu Lys Ser Phe Val
296 180 185 190
297 Val Thr Ser Val Val Ala Phe Pro Thr Asp Ser Lys Thr Val Gln Arg
298 195 200 205
299 Thr Gln Asp Asn Ser Cys Ser Phe Gly Leu His Ala Arg Gly Val Glu
300 210 215 220
301 Leu Met Arg Phe Thr Thr Pro Gly Phe Pro Asp Ser Pro Tyr Pro Ala
302 225 230 235 240
303 His Ala Arg Cys Gln Trp Ala Leu Arg Gly Asp Ala Asp Ser Val Leu
304 245 250 255
305 Ser Leu Thr Phe Arg Ser Phe Asp Leu Ala Ser Cys Asp Glu Arg Gly
306 260 265 270
307 Ser Asp Leu Val Thr Val Tyr Asn Thr Leu Ser Pro Met Glu Pro His

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VERIFICATION SUMMARY

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L:11 M:270 C: Current Application Number differs, Replaced Application Number  
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date